

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/811,080

Source: _____

Date Processed by STIC: _____

ENTERED



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/811,080

DATE: 10/18/2004

TIME: 10:03:39

Input Set : N:\Crf3\RULE60\10811080.raw.txt
 Output Set: N:\CRF4\10182004\J811080.raw

1 <110> APPLICANT: Gerritsen, Mary E.
 2 Goddard, Audrey
 3 Grimaldi, J. Christopher
 4 Mehraban, Fuad
 5 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES, THEIR NUCLEIC ACIDS, AND METHODS
 6 FOR THEIR USE IN ANGIOGENESIS AND VASCULARIZATION
 7 <130> FILE REFERENCE: P1776R2US
 8 <140> CURRENT APPLICATION NUMBER: US/10/811,080
 9 <141> CURRENT FILING DATE: 2004-03-26
 10 <150> PRIOR APPLICATION NUMBER: US/09/684,458
 11 <151> PRIOR FILING DATE: 2000-10-05
 12 <150> PRIOR APPLICATION NUMBER: US 60/158,587
 13 <151> PRIOR FILING DATE: 1999-10-07
 14 <150> PRIOR APPLICATION NUMBER: US 60/162,611
 15 <151> PRIOR FILING DATE: 1999-10-28
 16 <160> NUMBER OF SEQ ID NOS: 29
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 2891
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
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 gccgggcgtcccggttccctacatc cgcgtcccta ggcggccggcg 89
 Met Ala Phe Met Glu Lys Pro Pro
 26 1 5
 gcc ggc aag gtg ctg ctg gac gac acg gtg ccg ctg aca 128
 Ala Gly Lys Val Leu Leu Asp Asp Thr Val Pro Leu Thr
 29 10 15 20
 gca gcc atc gag gcg agc cag agc ctg cag tcc cac acg 167
 Ala Ala Ile Ala Ser Gln Ser Leu Gln Ser His Thr
 32 25 30
 gaa tat att att cga gtg caa aga gga att tct gtg gaa 206
 Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser Val Glu
 35 35 40 45
 aac agc tgg cag att gtt aga aga tac agt gac ttt gat 245
 Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp
 38 50 55 60
 ttg ctt aac aac agc tta cag att gca ggc cta agt cta 284
 Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu
 41 65 70
 cct ctt cct ccc aaa aaa ttg att ggt aac atg gat cgt 323
 Pro Leu Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg
 44 75 80 85

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45      gaa ttc ata gct gaa agg cag aaa ggt ctt cag aac tat 362
46      Glu Phe Ile Ala Glu Arg Gln Lys Gly Leu Gln Asn Tyr
47          90           95
48      ctc aac gtg atc aca aca aat cat atc ttg tct aat tgt 401
49      Leu Asn Val Ile Thr Thr Asn His Ile Leu Ser Asn Cys
50          100          105          110
51      gag ctg gtt aag aag ttt tta gat cca aac aac tat tcc 440
52      Glu Leu Val Lys Lys Phe Leu Asp Pro Asn Asn Tyr Ser
53          115          120          125
54      gca aac tat act gag att gcc ttg caa cag gtt tcc atg 479
55      Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln Val Ser Met
56          130          135
57      ttc ttc cga tca gaa cca aag tgg gag gtg gtg gaa cct 518
58      Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu Pro
59          140          145          150
60      ttg aaa gac ata ggt tgg aga ata agg aag aaa tat ttc 557
61      Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe
62          155          160
63      ttg atg aag att aaa aat cag cca aag gaa cgg cta gtg 596
64      Leu Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val
65          165          170          175
66      tta agc tgg gct gac ctt ggc cca gac aag tat ttg tca 635
67      Leu Ser Trp Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser
68          180          185          190
69      gat aaa gat ttt cag tgt cta atc aaa ctt ctg cct tct 674
70      Asp Lys Asp Phe Gln Cys Leu Ile Lys Leu Leu Pro Ser
71          195          200
72      tgt ttg cac cct tac atc tat cgg gtt acc ttt gcc aca 713
73      Cys Leu His Pro Tyr Ile Tyr Arg Val Thr Phe Ala Thr
74          205          210          215
75      gct aat gaa tcc tca gcg ttg cta att agg atg ttt aac 752
76      Ala Asn Glu Ser Ser Ala Leu Leu Ile Arg Met Phe Asn
77          220          225
78      gaa aag gga aca ttg aag gat ctg atc tac aag gca aaa 791
79      Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys Ala Lys
80          230          235          240
81      cca aaa gac cca ttt cta aag aag tac tgc aac cct aag 830
82      Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys
83          245          250          255
84      aag att cag ggc ctg gaa ctc cag caa ata aaa aca tat 869
85      Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr
86          260          265
87      gga cgg caa ata tta gag gta ctg aag ttt ctt cat gac 908
88      Gly Arg Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp
89          270          275          280
90      aag gga ttc cct tat ggg cat ctt cac gcc tcc aat gtg 947
91      Lys Gly Phe Pro Tyr Gly His Leu His Ala Ser Asn Val
92          285          290
93      atg ctc gat ggg gac act tgt cgg ctg ctg gac ctt gag 986

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94 Met Leu Asp Gly Asp Thr Cys Arg Leu Leu Asp Leu Glu
95 295 300 305
96 aat tcc tta ttg ggc ctg cct tcc ttc tac cga tct tat 1025
97 Asn Ser Leu Leu Gly Leu Pro Ser Phe Tyr Arg Ser Tyr
98 310 315 320
99 ttt tca caa ttc agg aaa atc aat aca ttg gaa agt gtg 1064
100 Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu Glu Ser Val
101 325 330
102 gat gtc cac tgc ttt ggc cac tta ctg tat gaa atg act 1103
103 Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met Thr
104 335 340 345
105 tat gga cga ccg cca gac tcg gtg cct gtg gac tcc ttc 1142
106 Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe
107 350 355
108 cct cct gcc ccg tcc atg gct gtg gtg gcc gtg ttg gag 1181
109 Pro Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu
110 360 365 370
111 tct acg ctg tct tgt gaa gcc tgt aaa aat ggc atg cct 1220
112 Ser Thr Leu Ser Cys Glu Ala Cys Lys Asn Gly Met Pro
113 375 380 385
114 acc atc tcc ccg ctc tta cag atg cca tta ttc agc gat 1259
115 Thr Ile Ser Arg Leu Leu Gln Met Pro Leu Phe Ser Asp
116 390 395
117 gtt tta cta acc act tct gaa aaa cca cag ttt aag atc 1298
118 Val Leu Leu Thr Thr Ser Glu Lys Pro Gln Phe Lys Ile
119 400 405 410
120 cct aca aag tta aaa gag gca ttg aga att gcc aaa gaa 1337
121 Pro Thr Lys Leu Lys Glu Ala Leu Arg Ile Ala Lys Glu
122 415 420
123 tgt ata gag aag aga cta att gag gaa cag aaa cag att 1376
124 Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys Gln Ile
125 425 430 435
126 cac cag cat cga aga ctg aca aga gct cag tcc cac cat 1415
127 His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His
128 440 445 450
129 gga tct gag gag gaa aga aaa aaa aga aag att tta gct 1454
130 Gly Ser Glu Glu Arg Lys Lys Arg Lys Ile Leu Ala
131 455 460
132 cga aag aag tca aaa cga tct gct ctt gaa aat agt gaa 1493
133 Arg Lys Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu
134 465 470 475
135 gag cat tca gcg agg tac agc aac tcc aat aat tca gga 1532
136 Glu His Ser Ala Arg Tyr Ser Asn Ser Asn Ser Gly
137 480 485
138 tct ggg gcc agc tca cct ctc acg tcc ccg tca tcg cca 1571
139 Ser Gly Ala Ser Ser Pro Leu Thr Ser Pro Ser Ser Pro
140 490 495 500
141 act cca ccc tct aca tca ggg ata tct gca tta cct cca 1610
142 Thr Pro Pro Ser Thr Ser Gly Ile Ser Ala Leu Pro Pro

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143	505	510	515
144	cct cct cca cct cca cca cca gca gct ccc ttg cct	1649	
145	Pro Pro Pro Pro Pro Pro Ala Ala Pro Leu Pro		
146	520	525	
147	cct gcg agc acc gag gta cct gcc cag ctc tcg tct cag	1688	
148	Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser Gln		
149	530	535	540
150	gct gtg aat ggc atg agc cga ggg gcc ttg ctc agc tcc	1727	
151	Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser		
152	545	550	
153	atc cag aat ttc caa aaa gga act ttg agg aaa gcc aaa	1766	
154	Ile Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys		
155	555	560	565
156	acc tgt gat cac agt gct ccg aag atc ggc tg aa	1800	
157	Thr Cys Asp His Ser Ala Pro Lys Ile Gly		
158	570	575	577
159	gttcctgtt tacacttggaa gggaaaagtt ctttttatt cctactcacc	1850	
160	cctacccccc aaactaccct ctccctggaa aagtaattgc tgagccagta	1900	
161	cagccacaaa cagtaactatt ttgcagatgc tcataatgc agctttcga	1950	
162	gagaataat tcttaagca gaataaagtt aggctggcat tgctccctta	2000	
163	agatcttgc tcttattaa ccctgtaaag gagtctgtt tatcctctaa	2050	
164	tggccaggct ttgggacag cagcatattt aatatatttc accaactaaa	2100	
165	ggaaatagac agaaaaacaa tgacaatatt caatcacagc agtaaatggc	2150	
166	cttgcgttg caatcccttc taacccatca gacagctcct agaaacattc	2200	
167	cttacagttc atttctctaa agcatttct gattcttaga taactccat	2250	
168	tttgcgtacc ttatcttag acattaacac tatagccaa agcatagtt	2300	
169	cttgcctaaa tcagaaagca actgagttct ttgtttctc ctcaaataaga	2350	
170	atggggAACG ttccacaacat tctcttaagt tctaacagga ataccattgt	2400	
171	gttatagaa ctcaggcgtg ctaaagcaac tactctagac ccatagttct	2450	
172	ttttagttag atgtattgaa acagacaaaa atattaacat cagaaaaagc	2500	
173	tcttgccaat tagaggatct tcttaatcct cagcaattaa gttgggggtt	2550	
174	tgaggggggc aggtcattgt tacaacagaa gtaaatttgg catctataga	2600	
175	aatcaattat gatTTTGAAGT agatttatct aaatataatca atatagcatc	2650	
176	tcttaatgt tagtcattta ttagaaagat cctttatcct gatttgctta	2700	
177	aacctttcaa taaattgcac tttaaaggat tataaataat ccatttaaaa	2750	
178	attcaagtac acacatcagt gttggttact atgcagagaa tgcattgtg	2800	
179	tatagttca tgtaatctgt tatgtcagct gtatTTTA ttaaaatcat	2850	
180	gtcaagaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa a	2891	
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183	<211> LENGTH: 577		
184	<212> TYPE: PRT		
185	<213> ORGANISM: Homo sapiens		
186	<400> SEQUENCE: 2		
187	Met Ala Phe Met Glu Lys Pro Pro Ala Gly Lys Val Leu Leu Asp		
188	1 5 10 15		
189	Asp Thr Val Pro Leu Thr Ala Ala Ile Glu Ala Ser Gln Ser Leu		
190	20 25 30		
191	Gln Ser His Thr Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser		
192	35 40 45		

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193	Val	Glu	Asn	Ser	Trp	Gln	Ile	Val	Arg	Arg	Tyr	Ser	Asp	Phe	Asp
194					50				55						60
195	Leu	Leu	Asn	Asn	Ser	Leu	Gln	Ile	Ala	Gly	Leu	Ser	Leu	Pro	Leu
196					65				70						75
197	Pro	Pro	Lys	Lys	Leu	Ile	Gly	Asn	Met	Asp	Arg	Glu	Phe	Ile	Ala
198					80				85						90
199	Glu	Arg	Gln	Lys	Gly	Leu	Gln	Asn	Tyr	Leu	Asn	Val	Ile	Thr	Thr
200					95				100						105
201	Asn	His	Ile	Leu	Ser	Asn	Cys	Glu	Leu	Val	Lys	Lys	Phe	Leu	Asp
202					110				115						120
203	Pro	Asn	Asn	Tyr	Ser	Ala	Asn	Tyr	Thr	Glu	Ile	Ala	Leu	Gln	Gln
204					125				130						135
205	Val	Ser	Met	Phe	Phe	Arg	Ser	Glu	Pro	Lys	Trp	Glu	Val	Val	Glu
206					140				145						150
207	Pro	Leu	Lys	Asp	Ile	Gly	Trp	Arg	Ile	Arg	Lys	Lys	Tyr	Phe	Leu
208					155				160						165
209	Met	Lys	Ile	Lys	Asn	Gln	Pro	Lys	Glu	Arg	Leu	Val	Leu	Ser	Trp
210					170				175						180
211	Ala	Asp	Leu	Gly	Pro	Asp	Lys	Tyr	Leu	Ser	Asp	Lys	Asp	Phe	Gln
212					185				190						195
213	Cys	Leu	Ile	Lys	Leu	Leu	Pro	Ser	Cys	Leu	His	Pro	Tyr	Ile	Tyr
214					200				205						210
215	Arg	Val	Thr	Phe	Ala	Thr	Ala	Asn	Glu	Ser	Ser	Ala	Leu	Ile	
216					215				220						225
217	Arg	Met	Phe	Asn	Glu	Lys	Gly	Thr	Leu	Lys	Asp	Leu	Ile	Tyr	Lys
218					230				235						240
219	Ala	Lys	Pro	Lys	Asp	Pro	Phe	Leu	Lys	Lys	Tyr	Cys	Asn	Pro	Lys
220					245				250						255
221	Lys	Ile	Gln	Gly	Leu	Glu	Leu	Gln	Ile	Lys	Thr	Tyr	Gly	Arg	
222					260				265						270
223	Gln	Ile	Leu	Glu	Val	Leu	Lys	Phe	Leu	His	Asp	Lys	Gly	Phe	Pro
224					275				280						285
225	Tyr	Gly	His	Leu	His	Ala	Ser	Asn	Val	Met	Leu	Asp	Gly	Asp	Thr
226					290				295						300
227	Cys	Arg	Leu	Leu	Asp	Leu	Glu	Asn	Ser	Leu	Leu	Gly	Leu	Pro	Ser
228					305				310						315
229	Phe	Tyr	Arg	Ser	Tyr	Phe	Ser	Gln	Phe	Arg	Lys	Ile	Asn	Thr	Leu
230					320				325						330
231	Glu	Ser	Val	Asp	Val	His	Cys	Phe	Gly	His	Leu	Leu	Tyr	Glu	Met
232					335				340						345
233	Thr	Tyr	Gly	Arg	Pro	Pro	Asp	Ser	Val	Pro	Val	Asp	Ser	Phe	Pro
234					350				355						360
235	Pro	Ala	Pro	Ser	Met	Ala	Val	Val	Ala	Val	Leu	Glu	Ser	Thr	Leu
236					365				370						375
237	Ser	Cys	Glu	Ala	Cys	Lys	Asn	Gly	Met	Pro	Thr	Ile	Ser	Arg	Leu
238					380				385						390
239	Leu	Gln	Met	Pro	Leu	Phe	Ser	Asp	Val	Leu	Leu	Thr	Thr	Ser	Glu
240					395				400						405
241	Lys	Pro	Gln	Phe	Lys	Ile	Pro	Thr	Lys	Leu	Lys	Glu	Ala	Leu	Arg

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 162,165,183,184,187,204,207,211,216,219,222,223,225,237,240

Seq#:5; N Pos. 244,250,253,262,267,269,275,279,282,289,290

Seq#:9; N Pos. 379,433,459,492,517,541,549,561,575,579,582,710,742,774,784

Seq#:13; N Pos. 103

Seq#:13; Xaa Pos. 11

Seq#:15; N Pos. 74,1306

Seq#:16; Xaa Pos. 104

Seq#:17; N Pos. 4,107,109,112,119,122,176,323,1616,1878,1881,1911,1924,1939

Seq#:17; N Pos. 1953,1982,1991,1992,2000,2443

Seq#:17; Xaa Pos. 18,449

Seq#:18; Xaa Pos. 18,448

Seq#:19; N Pos. 300

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:9; Line(s) 511

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10811080.raw.txt
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L:479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:150
M:341 Repeated in SeqNo=5
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:350
M:341 Repeated in SeqNo=9
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:91
M:341 Repeated in SeqNo=13
L:830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:50
M:341 Repeated in SeqNo=15
L:938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:90
L:982 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
M:341 Repeated in SeqNo=17
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:15
M:341 Repeated in SeqNo=18
L:1225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:250